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1748
U.S. DEPARTMENT OF COMMERCE
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SEARCH REQUEST FORM

Requestor's

Name: Anne-Marie Baker

Serial

Number: 08/963, 288

Date: 8/15/02

Phone: 306-9155

Art Unit: 1632

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please search nucleic acid databases for

: TTCTGA GAA .

I would like the search to be size-limited to less than 30 nucleotides (in other words, I don't want any hits for sequences over 30 nucleotides).

Note: The sequence is smaller than 10 nucleotides and therefore is not subject to compliance with the sequence rules.

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

STAFF USE ONLY

Date completed: 8-21-02

Searcher: PZB

Terminal time: 12

Elapsed time: prep 576

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

STIC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

IG

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

abs 06 Other

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model.

Run on: August 20, 2002, 21:33:29 ; search time 1861.18 seconds

(without alignments)
101.193 Million cell updates/sec

Title:

NA_SEQ

Perfect score:

9

Sequence:

ttctggaga 9

Scoring table:

IDENTITY_NUC

Gapop

10.0 , Gapext 1.0

Searched:

1797656 seqs, 10463268293 residues

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

gb_ba:*

gb_htg:*

gb_in:*

gb_com:*

gb_ov:*

gb_pat:*

gb_ph:*

gb_pl:*

gb_pr:*

gb_ro:*

gb_sts:*

gb_sy:*

gb_un:*

gb_vl:*

em_ba:*

em_fun:*

em_hum:*

em_in:*

em_lmu:*

em_lor:*

em_lov:*

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em_pl:*

em_ro:*

em_sts:*

em_lun:*

em_lv:*

em_htg_inv:*

em_htg_other:*

em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No. Score Match length DB ID Description

Query Match Similarity

Best Local Similarity 100.0%; Score 9; DB 6; Length 15;
pred. No. 1.2e+05;

RESULT	1	LOCUS	AR133394/	DEFINITION	Sequence 1819 from patent US 6194150.	LINEAR	PAT	16-MAY-2001
ACCESSION	AR133394	VERSION	AR133394.1	KEYWORDS	GI:14122299			
SOURCE		ORGANISM	Unknown.					
FEATURES		REFERENCE	Unclassified.					
ORIGIN		AUTHORS	1 (bases 1 to 15)					
		TITLE	Stinchcombe,D.T., Jarvis,T. and McSwiggen,J.					
		JOURNAL	Nucleic acid based inhibition of C40					
		PATENT	Patent: US 6194150-A 1819 27-FEB-2001;					
		FEATURES	Location/Qualifiers					
		SUMMARY	/organism="Unknown"					
BASE COUNT	5 a 3 c 3 g 4 t							

Matches 9; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

DEFINITION Sequence 100 from patent US 5814517.

ACCESSION AR043730

VERSION AR043730.1 GI:5964738

KEYWORDS

ORGANISM Unknown.

RESULT 2

QY 1 ttcttagaa 9
|||||||
Db 15 TTCTGAGAA 7

LOCUS AR133395

DEFINITION Sequence 1820 from patent US 6154150.

ACCESSION AR133395

VERSION AR133395.1 GI:14122300

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.

TITLE Nucleic acid based inhibition of CD40

JOURNAL Patent: US 6154150-A 1820 27-FEB-2001;

FEATURES Location/Qualifiers

source 1..15 /organism="unknown"

BASE COUNT 4 a 3 c 2 g 6 t

ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 9; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

DEFINITION Sequence 101 from patent US 5814517.

ACCESSION AR043731

VERSION AR043731.1 GI:5964739

KEYWORDS

ORGANISM Unknown.

RESULT 3

QY 1 ttctgagaa 9
|||||||
Db 12 TTCTGAGAA 4

LOCUS AX277553

DEFINITION Sequence 32 from Patent WO0177327.

ACCESSION AX277553

VERSION AX277553.1 GI:16604752

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct.

REFERENCE Artificial sequence.

AUTHORS Caulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.

TITLE The high bone mass gene of 11q13

JOURNAL Patent: WO 0177327-A 32 18-OCT-2001;

FEATURES Genome Therapeutics Corporation (US)

source 1..18 /organism="synthetic construct"
/db_xref="taxon:32630"
/note="Artificial sequence is a primer."

BASE COUNT 5 a 5 c 4 g 4 t

ORIGIN

Query Match 100.0%; Score 9; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 9; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

DEFINITION Sequence 1530 from Patent WO0130362.

ACCESSION AX130312

VERSION AX130312.1 GI:14136617

KEYWORDS

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 19)

AUTHORS Robbins,J.M. and Tritz,R.

TITLE Ribozyme therapy for the treatment of proliferative skin and eye

RESULT 4

QY 1 ttcttagaa 9
|||||||
Db 6 TTCTGAGAA 14

LOCUS AR043730

DEFINITION 19 bp

ACCESSION PAT 29-SEP-1999

VERSION

KEYWORDS

ORGANISM

DEFINITION	Sequence 21 from patent US 6159691.
ACCESSION	ARI20696
VERSION	ARI20696.1
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
RESULT	12
Query Match	100.0%; Score 9; DB 6; Length 20;
Best Local Similarity	100.0%; Pred. No. 1.2e+05;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ttctgagaa 9
Db	1 ttCTGAGAA 9
LOCUS	E03365
DEFINITION	Oligonucleotide for detection of human papilloma virus gene.
ACCESSION	E03365
VERSION	E03365.1 GI:2171582
KEYWORDS	JP 1992058888-A/2.
SOURCE	synthetic construct.
ORGANISM	artificial sequence.
REFERENCE	1 (bases 1 to 20)
AUTHORS	Yoshie, O. and Mak, I.H.
TITLE	OLIGONUCLEOTIDE FOR DETECTING HUMAN PAPILLOMA VIRUS GENE AND
JOURNAL	DETECTION METHOD USING THE SAME
COMMENT	SHIONOGI & CO LTD
OS	Artificial gene
OC	Artificial sequence; Genes.
PN	JP 1992058888-A/2
PD	25-FEB-1992
PF	28-JUN-1990
PI	YOSHIE OSAMU, MAKI HIDEO
PC	C12N15/11, C07H21/00, C12Q1/68, G01N33/569, G01N33/574; CC
FEATURES	strandedness: Single; CC topology: Linear; CC hypothetical: No; CC anti-sense: No; Location/Qualifiers
source	1. .20 /organism="synthetic construct" /db_xref="taxon:32630"
BASE COUNT	5 a 2 c 8 g 5 t
ORIGIN	
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Best Local Similarity	100.0%; Pred. No. 1.2e+05;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ttctgagaa 9
Db	4 TTCTGAGAA 12
LOCUS	AR040919
DEFINITION	Sequence 18 from patent US 5811238.
ACCESSION	AR040919
VERSION	AR040919.1 GI:5961415
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
RESULT	22
Query Match	100.0%; Score 9; DB 6; Length 22;
Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ttctgagaa 9
Db	13 TTCTGAGAA 21
LOCUS	AR040919
DEFINITION	Sequence 18 from patent US 5811238.
ACCESSION	AR040919
VERSION	AR040919.1 GI:5961415
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
RESULT	22
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Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ttctgagaa 9
Db	13 TTCTGAGAA 21
LOCUS	AR051826
DEFINITION	Sequence 18 from patent US 5830721.
ACCESSION	AR051826
VERSION	AR051826.1 GI:5975190
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
RESULT	14
Query Match	100.0%; Score 9; DB 6; Length 22;
Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ttctgagaa 9
Db	13 TTCTGAGAA 21
LOCUS	AR051826
DEFINITION	DNA mutagenesis by random fragmentation and reassembly
ACCESSION	AR051826
VERSION	AR051826.1 GI:5975190
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
RESULT	18
Query Match	100.0%; Score 9; DB 6; Length 22;
Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ttctgagaa 9
Db	13 TTCTGAGAA 21
LOCUS	AR115962
DEFINITION	Sequence 18 from patent US 6132970.
ACCESSION	AR115962
VERSION	AR115962.1 GI:14096284
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
RESULT	22
Query Match	100.0%; Score 9; DB 6; Length 22;
Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ttctgagaa 9
Db	13 TTCTGAGAA 21
LOCUS	AR115962
DEFINITION	Sequence 18 from patent US 6132970.
ACCESSION	AR115962
VERSION	AR115962.1 GI:14096284
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
RESULT	22
Query Match	100.0%; Score 9; DB 6; Length 22;
Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ttctgagaa 9
Db	4 TTCTGAGAA 12
LOCUS	PAT 29-SEP-1999
DEFINITION	Methods for generating polynucleotides having desired characteristics by iterative selection and recombination
ACCESSION	PAT 29-SEP-1999
VERSION	PAT 29-SEP-1999
KEYWORDS	
SOURCE	Stemmer, W.P.C. and Crameri, A.
ORGANISM	Unknown.
RESULT	22
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Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ttctgagaa 9
Db	13 TTCTGAGAA 21
LOCUS	PAT 16-MAY-2001
DEFINITION	Methods of shuffling polynucleotides
ACCESSION	PAT 16-MAY-2001
VERSION	PAT 16-MAY-2001
KEYWORDS	
SOURCE	Stemmer, W.P.C.
ORGANISM	Unknown.
RESULT	22
Query Match	100.0%; Score 9; DB 6; Length 22;
Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ttctgagaa 9
Db	4 TTCTGAGAA 12
LOCUS	PAT 16-MAY-2001
DEFINITION	Methods of shuffling polynucleotides
ACCESSION	PAT 16-MAY-2001
VERSION	PAT 16-MAY-2001
KEYWORDS	
SOURCE	Stemmer, W.P.C.
ORGANISM	Unknown.

FEATURES	Location/qualifiers
SOURCE	1..22
BASE COUNT	8 a /organism="unknown"
ORIGIN	4 c 3 g 7 t

Query Match 100.0%; Score 9; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY	1 ttttgagaa 9	
DB	13 TTTTGAGAA 21	

Search completed: August 20, 2002, 23:23:03
Job time: 6574 sec

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GenCore version 4.5

OM nucleic - nucleic search, using sw model
Run on: August 20, 2002, 22:26:44 ; Search time 206.01 Seconds
(without alignments)
75.007 Million cell updates/sec

Title: NA_SEQ
Perfect score: 9
Sequence: 1 ttcttgaa 9
scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1736436 seqs, 858457221 residues
total number of hits satisfying chosen parameters: 1662488
Minimum DB seq length: 0
Maximum DB seq length: 30
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
c 1	9	100.0	9 16 AAT14149	Cytokine responsive
c 2	9	100.0	9 17 AAT41583	Cytokine activated
c 3	9	100.0	9 19 AAV56876	Regulatory element
c 4	9	100.0	15 17 AAJ66325	Mouse B7-2 hammerhead ribozyme
c 5	9	100.0	15 17 AAJ66326	Mouse B7-2 hammerhead ribozyme
c 6	9	100.0	17 21 AAR02601	Hammerhead ribozyme
c 7	9	100.0	17 21 AAR02602	Hammerhead ribozyme
c 8	9	100.0	17 21 AAR02603	Hammerhead ribozyme
c 9	100.0	17 21 AAR36041	Human genomic SNP	

SUMMARIES

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

PT detecting the presence of transcriptional regulatory protein in a sample
 XX
 PS Claim 7; Page 125; 135pp; English.
 CC The present oligonucleotide comprises a regulatory element TT^xNNAA, where x is 4-7, and the regulatory element binds an activated transcriptional regulatory protein in response to a signalling mol., i.e. a cytokine. This cytokine responsive DNA spacer regulatory element can be used to detect the presence of a transcriptional regulatory protein in a sample, and in assays for (ant)agonists of gene transcription. The identified cpos. may be used to treat cytokine-induced disease states, or to ameliorate disease states caused by cytokine deficiency, e.g. inflammation, anaemia, cytopenia and (pre)cancerous conditions.

SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100 0%; Score 9; DB 16; Length 9;
 Best Local Similarity 100 0%; Pred. No. 1.9e+08; ID: AAV58876 standard; DNA; 9 BP.
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttccatggaa 9
 YY 1 ttccatggaa 9
 Db 9 TTCTGAGAA 1

RESULT 2

ID AAT41583/C
 AT AAT41583 standard; DNA; 9 BP.
 XX

AC AAT41583;

XX DT 04-JUN-1997 (first entry)

DE Cytokine activated STAT protein dependent DNA regulatory element.

XX KW Regulatory element; protein; cytokine; responsive; host cell; transfection; agonist; antagonist; mediated; transcription; modulation; STAT; STAT5; STAT6; signalling pathway; ss.

XX OS Synthetic.

XX PN WO9630515-A1.

XX PD 03-OCT-1996.

XX PP 25-MAR-1996; 96WO-0504012.

XX PR 27-MAR-1995; 95US-0411020.

XX PA (LIGA-) LIGAND PHARM INC.

XX PI Lamb IP, Seidel HM;

XX DR WPI; 1998-541763/46.

XX PT Disclosure; Column 11; 58pp; English.

XX CC AAV5842-v56976 and AAV61601-w61631 are oligonucleotides used in the production of constructs comprising a cytokine-responsive regulatory element linked to a promoter which is linked to a heterologous coding sequence so that the coding sequence is under the transcriptional control of the regulatory element and the promoter, where the regulatory element has a nucleotide sequence selected from TTTCNNAA, TTANNTAA, and TTCNNNTAA where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to detect or isolate transcription-regulating proteins, e.g. STAT proteins, in a sample by contacting the sample with the construct so that the protein binds to the regulatory element, and detecting or separating the resulting complex. The cells can be used in screening assays for agonists of gene transcription, in which the level of expression of the coding sequence is measured in the presence and absence of a test compound or in the presence of the corresponding cytokine.

XX CC Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;
 CC DNA construct can be used to measure the ability of a compound to
 CC claim 5; Page 61; 72pp; English.

CC A novel DNA construct comprises an oligonucleotide (ON) comprising a regulatory element having the present sequence, operably linked to a promoter, which is operably linked to a heterologous gene (preferably a marker gene). The gene is under the transcriptional control of the promoter and the ON sequence when the ON is bound by a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF, erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9, IL-13 or IL-15. Cytokine responsive host cells transfected with the

CC act as an agonist or antagonist of cytokine mediated gene transcription. In particular, they can be used to screen for cytokine modulators involved in the STAT5 and/or STAT6 protein signalling pathway.

Query Match 100 0%; Score 9; DB 17; Length 9;
 Best Local Similarity 100 0%; Pred. No. 1.9e+08; ID: AAV58876 standard; DNA; 9 BP.
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttccatggaa 9
 YY 1 ttccatggaa 9
 Db 9 TTCTGAGAA 1

RESULT 3

ID AAV58876/C
 AT AAV58876;
 XX

XX DT 02-DEC-1998 (first entry)

DE Regulatory element containing oligonucleotide #35.

XX KW Cytokine-responsive regulatory primer; promoter; detection; isolation;

XX OS transcriptional control; STAT protein; screening; agonist; ss.

XX SYNTHETIC.

XX PN US584517-A.

XX PD 29-SEP-1998.

XX PP 27-MAR-1995; 95US-0410779.

XX PR 27-MAR-1995; 95US-0410779.

XX PR 14-APR-1994; 94US-0228935.

XX PA (LIGA-) LIGAND PHARM INC.

XX PI Lamb IP, Seidel HM;

XX DR WPI; 1998-541763/46.

XX PT DNA constructs containing cytokine-responsive regulatory elements - useful in assays for transcription-regulating proteins or gene transcription agonists or antagonists

XX PS Disclosure; Column 11; 58pp; English.

XX CC AAV5842-v56976 and AAV61601-w61631 are oligonucleotides used in the production of constructs comprising a cytokine-responsive regulatory element linked to a promoter which is linked to a heterologous coding sequence so that the coding sequence is under the transcriptional control of the regulatory element and the promoter, where the regulatory element has a nucleotide sequence selected from TTTCNNAA, TTANNTAA, and TTCNNNTAA where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to detect or isolate transcription-regulating proteins, e.g. STAT proteins, in a sample by contacting the sample with the construct so that the protein binds to the regulatory element, and detecting or separating the resulting complex. The cells can be used in screening assays for agonists of gene transcription, in which the level of expression of the coding sequence is measured in the presence and absence of a test compound or in the presence of the corresponding cytokine.

XX Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;
 CC DNA construct can be used to measure the ability of a compound to

CC in a recipient to an alloantigen of a donor. They can also be used for enhancing graft tolerance or for treating autoimmune disease, and for treating allergies and other inflammatory conditions. The RNA's can also be used in diagnosis. Ribozyme therapy impacts on the expression of gene expression which accompany treatment with retinoids and dexamethasone. CC The concentration of ribozyme required to affect a therapeutic treatment is lower than that required of antisense molecules, and is highly specific. The present sequence is used in the exemplification of the present invention.

XX Sequence 15 BP; 4 A; 3 C; 2 G; 6 U; 0 other;

Query Match Similarity 100.0%; Score 9; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+03; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctcqagaa 9
Db 16 TTCTGAGAA 8

RESULT 7
AAF02602/C
ID AAF02602 standard; DNA; 17 BP.
XX
AC AAF02602;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #897.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW Interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO20061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT protein, interferon alpha and erythropoietin -
XX
PS Claim 37; Page 76; 164pp; English.

XX
CC The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EGR3/COP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP). Inhibition of the repressors removes prevents the production (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
XX
PS Claim 37; Page 76; 164pp; English.

The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EGR3/COP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP). Inhibition of the repressors removes prevents the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.

XX
Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 other;

Query Match Similarity 100.0%; Score 9; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.5e+03; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctcqagaa 9
Db 15 TTCTGAGAA 7

RESULT 8
AAF02603/C
ID AAF02603 standard; DNA; 17 BP.
XX
AC AAF02603;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #898.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;

Query Match Similarity 100.0%; Score 9; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.5e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 17 BP; 5 A; 4 C; 4 G; 4 T; 0 other;

KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 WO200061725-A2.
 PN
 PT
 XX 19-OCT-2000.
 PD
 XX 11-APR-2000; 2000WO-US09721.
 PF
 XX 12-APR-1999; 99US-0129390.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 PI Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, Interferon alpha and erythropoietin
 XX PS Claim 37; Page 76; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EGR3/COPP-TF-1, the GATA
 CC transcription factor gene, IRF-2, and/or the CAMP Displacement
 CC protein (CDP). Inhibition of the repressors removes prevents prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XX SQ Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 other;
 CC
 CC Query Match 100.0%; Score 9; DB 21; Length 17;
 CC Best Local Similarity 100.0%; Pred. No. 9 5e+03;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 1 ttcttgagaa 9
 CC |||||||
 DB 13 TTTCTTGAGAA 5
 CC
 RESULT 9
 AAA36041 ID AAA36041 standard; DNA; 17 BP.
 AC AAA36041;
 XX DT 26-JUL-2000 (first entry)
 DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:98.
 KW Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
 KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
 KW genomic classification; identification; DNA fingerprinting;
 KW tumour characterisation; hybridisation; ss.
 XX OS Homo sapiens.
 XX PN WO2000188960-A2.
 PD 06-APR-2000.
 XX 24-SEP-1999; 99WO-US22263.
 XX 25-SEP-1998; 98US-0101757.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX PI Landers JE, Jordan B, Housman DE, Charest A;
 XX
 DR WPI; 2000-293181/25.
 XX
 PT detection of single nucleotide polymorphisms in genomes by preparation
 PT and analysis of reduced complexity genomes, useful for genotyping,
 PT fingerprinting and determining allele frequency of SNPs -
 XX
 PS Disclosure; Page 56; 111pp; English.
 CC A method has been developed for detecting the presence or absence of a
 CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
 CC method comprises preparing a reduced complexity genome (RCG) from the
 CC genomic sample and analysing the RCG for the presence or absence of a
 CC SNP allele. The method can be used to characterise a tumour, to generate
 CC a genomic pattern for an individual genome or to generate a genomic
 CC classification code for a genome. The method can be used to assess
 CC whether a subject is at risk for developing a disease or to identify a
 CC set of SNP alleles associated with a disease. The method can also be
 CC used to perform linkage analysis. AAA35944 to AAA35947 represent
 CC sequences used in the exemplification of the present invention. AAA35948
 CC to AA36632 represent nucleotide sequences containing SNPs.
 XX SQ Sequence 17 BP; 4 A; 1 C; 4 G; 8 T; 0 other;
 CC
 CC Query Match 100.0%; Score 9; DB 21; Length 17;
 CC Best Local Similarity 100.0%; Pred. No. 9.5e+03;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 1 ttcttgagaa 9
 CC |||||||
 DB 1 ttcttgagaa 9
 CC
 RESULT 10
 AAV24227/c
 ID AAV24227 standard; DNA; 18 BP.
 XX AC AAV24227;
 XX DT 12-AUG-1998 (first entry)
 DE Primer alpha(1)a for human alphoid DNA sequence.
 KW CENP-B box; mammalian artificial chromosome; MAC; chromosome 21;
 KW mammalian telomere; centromere; yeast artificial chromosomes; YAC;
 KW somatic gene therapy; PCR primer; ss.
 XX OS Synthetic.
 XX Homo sapiens.
 XX PN WO9808964-A1.
 PD 05-MAR-1998.
 XX PF 26-AUG-1996; 96WO-JP02381.
 XX PR 26-AUG-1996; 96WO-JP02381.
 XX PA (KENO/) IKENO M.
 PA (MASU/) MASUMOTO H.
 PA (OKAZAKI) OKAZAKI T.
 XX DR WPI; 1998-216941/19.
 XX Cooke RJ, Grimes BR, Ikeno M, Masumoto H, Okazaki T;
 PT
 PT Mammalian artificial chromosomes - prepared using DNA construct
 PT comprising mammalian telomere and centromere containing copies of
 PT CENP-B box sequences
 XX PS Disclosure; Page 34; 95pp; English.

CC This sequence is a primer for a human alphoid DNA sequence that can be used in the DNA construct of the invention. The construct is a mammalian artificial chromosome (MAC), and comprises a mammalian telomere and a centromere, where the centromere has a DNA sequence containing copies of the CENP-B box sequence. The invention also relates to methods for establishing yeast artificial chromosomes ('YACs') comprising mammalian telomeres and centromeres. The method can be used to construct, modify and stably maintain YACs in yeast cells which have the ability to form MACs when introduced into mammalian cells. The MACs can replicate autonomously, be stably maintained extrachromosomally and transmitted efficiently in mammalian cells. The MACs can be used for basic studies on organisation and function of mammalian chromosomes and also as a vector to introduce DNA segments (genes) of interest to test their functions in mammalian cells or bodies, since the genes carried by MACs will neither be subject to variable expression due to integration position effect nor cause unpredictable insertion mutation on host chromosomes. Furthermore MACs will have the capacity to accommodate a DNA segment up to megabases where an entire large gene or group of genes and regulatory elements could be included. The MACs can be used for somatic gene therapy or to generate transgenic mice.

Sequence 18 BP; 8 A; 4 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.6e+03; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttcttgagaa 9
||| | | | |
Db 18 TCTCGAGAA 10

RESULT 11

AAV24228 ID AAV24228 standard; DNA; 18 BP.

XX AC AAV24228;

XX DT 12-AUG-1998 (first entry)

DE Primer Alpha(1)B for human alphoid DNA sequence.

XX KW CENP-B box; mammalian artificial chromosome; MAC; chromosome 21; KW mammalian telomere; centromere; yeast artificial chromosomes; YAC; KW somatic gene therapy; PCR primer; ss.

XX OS Synthetic.

OS HOMO sapiens.

XX PN WO9808964-A1.

XX PD 05-MAR-1998.

XX PF 26-AUG-1996; 96W0-JP02381.

XX PR 26-AUG-1996; 96W0-JP02381.

XX PA (KENO/) IKENO M.

PA (MASU/) MASUMOTO H.

PA (OKAZ/) OKAZAKI T.

XX PI Cooke HJ, Grimes BR, Ikeno M, Masumoto H, Okazaki T;

XX DR WPI; 1998-216941/19.

XX PT Mammalian artificial chromosomes - prepared using DNA construct comprising mammalian telomere and centromere containing copies of CENP-B box sequences

XX PS Disclosure: Page 34; 95pp; English.

CC This sequence is a primer for a human alphoid DNA sequence that can be

CC used in the DNA construct of the invention. The construct is a mammalian CC artificial chromosome (MAC), and comprises a mammalian telomere and a CC centromere, where the centromere has a DNA sequence containing copies of CC the CENP-B box sequence. The invention also relates to methods for CC establishing yeast artificial chromosomes ('YACs') comprising mammalian CC telomeres and centromeres. The method can be used to construct, modify CC and stably maintain YACs in yeast cells which have the ability to form CC MACs when introduced into mammalian cells. The MACs can replicate CC autonomously, be stably maintained extrachromosomally and transmitted CC efficiently in mammalian cells. The MACs can be used for basic studies on CC organisation and function of mammalian chromosomes and also as a vector CC to introduce DNA segments (genes) of interest to test their functions in CC mammalian cells or bodies, since the genes carried by MACs will neither CC be subject to variable expression due to integration position effect nor CC cause unpredictable insertion mutation on host chromosomes. Furthermore CC MACs will have the capacity to accommodate a DNA segment up to megabases CC where an entire large gene or group of genes and regulatory elements CC could be included. The MACs can be used for somatic gene therapy or to CC generate transgenic mice.

Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 9; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.6e+03; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttcttgagaa 9
||| | | | |
Db 1 ttcttgagaa 9

RESULT 12

ABA82404 ID ABA82404 standard; DNA; 18 BP.

XX AC ABA82404;

XX DT 25-JAN-2002 (first entry)

DE HBML polymorphism containing amplicon PCR primer 1863F.

XX KW Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3; KW antiresorbive therapy; vaccine; bone disorder; Paget's disease; adapter; KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO20177327-A1.

XX PD 18-OCT-2001.

XX PF 21-JUN-2000; 2000WO-US16951.

XX PR 05-APR-2000; 2000US-054371.

XX PR 05-APR-2000; 2000US-0544398.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PT Carulli JP, Little RD, Recker RR, Johnson ML;

XX DR WPI; 2001-657171/75.

XX PT New high bone mass (HBM) and zmax1 genes and proteins useful for modulating bone mass for the treatment of e.g. osteoporosis -

XX PS Disclosure: Page 63; 44pp; English.

XX CC The present invention describes the human Zmax1 gene and the high bone CC mass (HBM) gene which are found on chromosome 11q13.3. The Zmax1 and CC HBM genes have osteoplastic activities. The genes can be used in gene CC

CC therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia. ABA82038 to ABA82700 and AAC80168 to AAC68193 represent sequences used in the exemplification of the present invention.

Db 6 ttctqaga 14

SQ sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 other;

```

Query Match      100.0%; Score 9; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY	1	ttctgagaa	9
Db	6	ttctgagaa	14

RESULT 13
ABA82646

ID ABAB2
XX
AC
ABA82

AC XX
XX DT 25-JAN-2002 (first entry)
XX DE Human Zmax1 PCR primer SEQ ID NO:32..
AKROZ040;

XX
KW Human; high bone mass; HBM gene; Zimata sequence tagged site; SMC; osteoclast

KW antisense tagged site; **SIS**; osteoporosis; osteopathic; gene therapy;
KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; SSS

XX
OS
OS
Homo sapiens.
Synthetic.

WO200177327-A1.

XX
PD
XX 18-OCT-2001.

PF 21-JUN-2000; 2000WO-US16951.
XX
PR 05-APR-2000: 2000US-054371.

PR 05-APR-2000; 2000US-0544398.
XX

PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Carulli JP, Little RD, Recker R

XX
DR
YY
WPI: 2001-657171/75.

PT
New high bone mass (HBM) and *Zmax1* genes and
modulating bone mass for the treatment of e.g.

XX
PS Disclosure; Page 103; 443pp; English.
XX

CC
CC The present invention describes the human *Zmax1* gene and the high bone mass (HBM) gene which are found on chromosome 11q13.3. The *Zmax1* and

CC genes have osteoclast activities. The genes can be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibro dysplasia. ABAB2038 to ABAB2700 and AAGC1618 to AAGC6819 represent sequences used in the exemplification of the present invention.

Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 other;

Query Match: 100.0%; Score: 9; DB: 22; Length: 18;

Best Local Similarity 100.0%; Pred. No. 9.6e+03; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 ttctgagaa 9

RESULT 15
 AAV56941/C
 ID AAV56941 standard; DNA; 19 BP.
 XX
 AC AAV56941;
 XX 02-DEC-1998 (First entry)
 DE Regulatory element containing oligonucleotide #100.
 XX
 KW Cytokine-responsive regulatory; primer; promoter; detection; isolation;
 XX transcriptional control; STAT protein; screening; agonist; ss.
 OS Synthetic.
 XX
 PN US5814517-A.
 XX
 PD 29-SEP-1998.
 XX
 PP 27-MAR-1995; 95US-0410779.
 XX
 PR 27-MAR-1995; 95US-0410779.
 PR 14-APR-1994; 94US-0228935.
 XX
 PA (LIGA-) LIGAND PHARM INC.
 XX
 PI Lamb LP, Seidel HM;
 XX
 DR WPI; 1998-541763/46.
 XX
 PT DNA constructs containing cytokine-responsive regulatory elements -
 PT useful in assays for transcription regulating proteins or gene
 PT transcription agonists or antagonists
 XX
 PS Example 1; Column 19-20; 58pp; English.
 XX
 CC AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
 CC production of constructs comprising cytokine-responsive regulatory
 CC element linked to a promoter which is linked to a heterologous coding
 sequence so that the coding sequence is under the transcriptional
 CC control of the regulatory element and the promoter, where the regulatory
 CC element has a nucleotide sequence selected from TTCNNGAA, TTNNYAA, and
 CC TTTCNYYAA where N is A, T, C or G, and Y = 3 or 4. The constructs can be
 CC used to detect or isolate transcription-regulating proteins, e.g. STAT
 CC proteins, in a sample by contacting the sample with the construct so that
 CC the protein binds to the regulatory element, and detecting or separating
 CC the resulting complex. The cells can be used in screening assays for
 CC agonists of gene transcription, in which the level of expression of the
 CC coding sequence is measured in the presence and absence of a test
 CC compound or in the presence of the corresponding cytokine.
 XX
 Sequence 19 BP; 4 A; 5 C; 4 G; 6 T; 0 other;
 SQ

Query	Match	Score	DB	Length
Qy	ttcgtggaa	9	19	19
Db	ttcgagaa	8		

Best Local Similarity 100.0%; Score 9; DB 19; Length 19;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: August 20, 2002, 23:27:54
 Job time: 3670 sec

GenCore version 4.5
 copyright (c) 1993 - 2000 Compugen Ltd.

M nucleic - nucleic search, using sw model

un on: August 20, 2002, 22:19:24 ; Search time 43.04 Seconds
 (without alignments)
 51.364 Million cell updates/sec

title: perfect score: 9
 sequence: 1 ttctgagaa 9
 scoring table: IDENTITY-NUC
 Gapop 10.0 , Gapext 1.0

searched: 383533 seqs, 122816752 residues

total number of hits satisfying chosen parameters:
 minimum DB seq length: 0
 maximum DB seq length: 30

post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

database :

Issued Patents NA: *

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 2: /cggn2_6/pctodata/2/inav5B_COMB.seq: *
 3: /cggn2_6/pctodata/2/inav6A_COMB.seq: *
 4: /cggn2_6/pctodata/2/inav6B_COMB.seq: *
 5: /cggn2_6/pctodata/2/inav/PCTUS_COMB.seq: *
 6: /cggn2_6/pctodata/2/inav/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Length	DB ID	Description
c 1	9	100.0	9 1	Sequence 13, Appl
c 2	9	100.0	9 1	US-08-411-020-13
c 3	9	100.0	9 1	US-08-410-779B-35
c 4	9	100.0	9 2	US-08-852-091-34
c 5	9	100.0	9 3	PCT-US95-17025-34
c 6	9	100.0	9 5	PCT-US95-17025-34
c 7	9	100.0	15 2	US-08-585-604B-1820
c 8	9	100.0	15 4	US-09-038-073-1820
c 9	9	100.0	15 4	US-09-038-073-1820
c 10	9	100.0	19 4	US-09-038-073-1820
c 11	9	100.0	19 5	US-08-411-020-57
c 12	9	100.0	19 1	US-08-410-779B-100
c 13	9	100.0	19 1	US-08-410-779B-100
c 14	9	100.0	19 1	US-08-410-779B-100
c 15	9	100.0	19 5	PCT-US95-04477-100
c 16	9	100.0	19 5	PCT-US95-04477-101
c 17	9	100.0	20 2	US-08-415B-21
c 18	9	100.0	20 3	US-09-078-317-7
c 19	9	100.0	20 3	US-08-600-982-20
c 20	9	100.0	20 5	PCT-US94-10201A-20
c 21	9	100.0	22 1	US-08-198-431-18
c 22	9	100.0	22 1	US-08-223-415B-21
c 23	9	100.0	22 2	US-08-537-874-18
c 24	9	100.0	22 3	US-08-929-10-13
c 25	9	100.0	22 3	US-08-821-899-18
c 26	9	100.0	22 3	US-09-100-850A-18

RESULT 1
 US-08-411-020-13/C

SEQUENCE 13, Application US/08411020
 Sequence No. 5712094

GENERAL INFORMATION:

APPLICANT: SEIDEL, H. MARTI
 APPLICANT: LAMB, I. PETER
 APPLICANT: CHAN, SHIN-SHAY TIAN

TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR DETECTING MODULATORS OF CYTOKINE ACTION

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ligand Pharmaceuticals Incorporated
 STREET: 9393 Towne Centre Drive
 CITY: San Diego
 STATE: California
 COUNTRY: US
 ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/411,020
 FILING DATE: 27-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jurgenssen, Thomas E.
 REGISTRATION NUMBER: 34,195
 REFERENCE/DOCKET NUMBER: 016-0030.US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 550-7675
 TELEFAX: (619) 535-3006

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
 DESCRIPTION: SYNTHETIC DNA"
 US-08-411-020-13

ALIGNMENTS

Query Match 100.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 2
 US-08-369-796-34/c
 ; Sequence 34, Application US/08369796
 ; Patent No. 5716622
 ; GENERAL INFORMATION:
 ; APPLICANT: James E. Darnell, Jr.
 ; APPLICANT: Zilong Wen
 ; APPLICANT: Zhong Zhong
 ; ADDRESSEE: Curt M. Horvath
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/08410,779B
 ; FILING DATE: 27-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION NUMBER: US 08/228,935
 ; APPLICATION NUMBER: US/08369,796
 ; FILING DATE: 06-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-116
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = OTHER NUCLEIC ACID,
 ; DESCRIPTION: SYNTHETIC DNA,
 ; US-08-410-779B-35
 ;
 RESULT 4
 US-08-852-091-34/c
 ; Sequence 34, Application US/08852091
 ; Patent No. 5893228
 ; GENERAL INFORMATION:
 ; APPLICANT: James E. Darnell, Jr.
 ; APPLICANT: Zilong Wen
 ; APPLICANT: Curt M. Horvath
 ; APPLICANT: Zhong Zhong
 ; ADDRESSEE: Curt M. Horvath
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/852,091
 ; FILING DATE: 06-MAY-1997

Query Match 100.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ttctgagaa 9
 |||||
 Db 9 TTCTGAGAA 1

RESULT 3
 US-08-410-779B-35/C
 ; Sequence 35, Application US/08410779B
 ; Patent No. 5814517
 ; GENERAL INFORMATION:
 ; APPLICANT: Seidel, R. Maruti
 ; APPLICANT: Lamb, I. Peter
 ; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS FOR THEIR USE
 ; NUMBER OF SEQUENCES: 166
 ; CORRESPONDENCE ADDRESS:

CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/369,796
 FILING DATE: 06-JAN-1995
 ATTORNEY / AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 343-1684
 TELEFAX: 201 487-5800
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA synthetic probe
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-852-091-34

Query Match 100.0%; Score 9; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttctggaa 9
 ||||| |||
 Db 9 TTCTGAGA 1

RESULT 5
 PCT-US95-04477-35/C
 Sequence 35, Application PC/US9504477
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
 NUMBER OF SEQUENCES: 165
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Patentin Release #1.0, version #1.30 (BPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04477
 FILING DATE: 14-APR-1994
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/369,796
 FILING DATE: 06-JAN-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-116
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA synthetic probe
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 PCT-US95-17025-34

Query Match 100.0%; Score 9; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttctgagaa 9
 ||||| |||
 Db 9 TTCTGAGA 1

RESULT 7
 US-08-505-684B-1819/C
 Sequence 1819, Application US/08585684B
 PATENT NO. 5877021
 GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Daniel T.
 APPLICANT: Jarvis, Thale
 APPLICANT: McSwiggen, James
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE INDUCTION OF GRAFT TOLERANCE AND REVERSAL OF IMMUNE RESPONSES
 NUMBER OF SEQUENCES: 2751

Query Match 100.0%; Score 9; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttctgagaa 9
 ||||| |||
 Db 9 TTCTGAGA 1

CORRESPONDENCE ADDRESS:
 ADDRESSE: Lyon & Lyon
 STREET: 633 West Fifth Street
 SUITE: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 1.5
 APPLICATION NUMBER: 60/000,951
 FILING DATE: January 16, 1996
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REFERENCE/DOCKET NUMBER: 32, 327
 REGISTRATION NUMBER: 32, 327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 1819:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 STRANDEDNESS: single
 TYPE: nucleic acid
 TOPOLOGY: linear
 US-08-585-684B-1819

RESULT 8
 US-08-585-684B-1820/c
 ; Sequence 1819, Application US/08585684B
 ; Parent No. 5877021
 GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Daniel T.
 APPLICANT: Jarvis, Thale
 APPLICANT: Moswigen, James
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: INDUCTION OF IMMUNE RESPONSES
 NUMBER OF SEQUENCES: 2/5,1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/038,073
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/585,684
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REFERENCE/DOCKET NUMBER: 32, 327
 REGISTRATION NUMBER: 32, 327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 1819:
 SEQUENCE CHARACTERISTICS:

RESULT 9
 US-09-038-073-1819/c
 ; Sequence 1819, Application US/09038073
 ; Patent No. 6194150
 GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Daniel T.
 APPLICANT: Jarvis, Thale
 APPLICANT: Moswigen, James
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: INDUCTION OF IMMUNE RESPONSES
 NUMBER OF SEQUENCES: 2/5,1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/038,073
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/585,684
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REFERENCE/DOCKET NUMBER: 32, 327
 REGISTRATION NUMBER: 32, 327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 1819:
 SEQUENCE CHARACTERISTICS:

RESULT 10
 Query Match 100.0%; Score 9; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 TOPOLGY: linear

QY 1 ttctgagaa 9
 Db 15 TCTGAGAA 7

RESULT 10
 US-09-038-073-1820/c
 Sequence 1820, Application US/09038073
 GENERAL INFORMATION:
 Patent No. 6194150
 APPLICANT: Stinchcomb, Daniel T.
 APPLICANT: Jarvis, Thale
 APPLICANT: McSwiggen, James
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 INDUCTION OF GRAFT TOLERANCE
 TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
 NUMBER OF SEQUENCES: 2751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: US
 ZIP: 90011
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/411,020
 FILING DATE: 27-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jurdensen, Thomas E.
 REGISTRATION NUMBER: 34,195
 REFERENCE/DOCKET NUMBER: 016-0030.US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 550-7675
 TELEFAX: (619) 535-3906
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
 SYNTHETIC DNA"
 US-08-411-020-56

RESULT 11
 US-08-411-020-56/c
 Sequence 56, Application US/08411020
 GENERAL INFORMATION:
 Patent No. 5712094
 APPLICANT: SEIDEL, H. MARTI
 APPLICANT: LAMB, I. PETER
 APPLICANT: CHAN, SHIN SHAY TIAN
 TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ligand Pharmaceuticals Incorporated
 STREET: 9393 Towne Centre Drive
 CITY: San Diego
 STATE: California
 COUNTRY: US

RESULT 12
 US-08-411-020-57
 Sequence 57, Application US/08411020
 GENERAL INFORMATION:
 Patent No. 5712094
 APPLICANT: SEIDEL, H. MARTI
 APPLICANT: LAMB, I. PETER
 APPLICANT: CHAN, SHIN SHAY TIAN
 TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ligand Pharmaceuticals Incorporated
 STREET: 9393 Towne Centre Drive
 CITY: San Diego
 STATE: California
 COUNTRY: US

Query Match 100.0%; Score 9; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 TOPOLGY: linear

QY 1 ttctgagaa 9
 Db 12 TCTGAGAA 4

US-09-038-073-1820
 Sequence 1820
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLGY: linear

US-09-038-073-1820
 Sequence 1820
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLGY: linear

US-09-038-073-1820
 Sequence 1820
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLGY: linear

ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/411,020
 FILING DATE: 27-MAR-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Jurgensen, Thomas E.
 REFERENCE/DOCKET NUMBER: 016-0030.US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 550-7675
 TELEFAX: (619) 535-3906

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
 SYNTHETIC DNA"
 US-08-411-020-57

Query Match 100 0%; Score 9; DB 1; Length 19;
 Best Local Similarity 100 0%; Pred. No. 1e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctbagaa 9
 |||||||||
 Db 8 TTCTGAGAA 16

RESULT 13
 US-08-410-779B-100/C
 Sequence 100, Application us/08410779B

PARENT NO. 5814517
 GENERAL INFORMATION:
 APPLICANT: SEDEL, H. MARTI
 APPLICANT: LAMB, I. PETER
 TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
 TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
 NUMBER OF SEQUENCES: 166

NUMBER OF SEQUENCES: 166

CORRESPONDENCE ADDRESS:
 ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
 STREET: 9393 TOWNE CENTRE DRIVE
 CITY: SAN DIEGO
 STATE: CALIFORNIA
 COUNTRY: US
 ZIP: 92121

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/410,779B
 FILING DATE: 27-MAR-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/228,935
 FILING DATE: 14-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: JURGENSEN, THOMAS E
 REFERENCE/DOCKET NUMBER: 34,195
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 550-7675
 TELEFAX: (619) 535-3906

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
 SYNTHETIC DNA"
 US-08-410-779B-101

Query Match 100 0%; Score 9; DB 1; Length 19;
 Best Local Similarity 100 0%; Pred. No. 1e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttcttgagaa 9
| ||| | | |
Db 8 TTTCTGAGAA 16

RESULT 15
PCT-US95-04477-100/C
; Sequence 100, Application PC/PCTUS9504477
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
; NUMBER OF SEQUENCES: 165
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
; PCT-US95-04477-100

Query Match 100.0%; Score 9; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ttcttgagaa 9
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Db 16 TTTCTGAGAA 8

Search completed: August 20, 2002, 23:24:06
Job time: 3882 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.									
OM nucleic - nucleic search, using sw model									
Run on: August 20, 2002, 21:26:14 ; Search time 1559.67 Seconds (without alignments) 77.884 Million cell updates/sec									
Title: D19956 RUMGSS09656 Perfect score: 12 A2424145 Sequence: 1 A2343355 IM0756114 scoring table: IDENTRY_NDC A2357286 IM0989117 Gapop 10.0 , Gapext 1.0 A2446127 IM024219 A2579569 IM0367112 Searched: 13736207 seqs, 6748477542 residues A2596866 IM040915015 A247556 T_brucei AL47556 T_brucei Total number of hits satisfying chosen parameters: 28088 A260957 IM04340606 Minimum DB seq length: 0 A251459 IM0361001 Maximum DB seq length: 30 A260286 IM04205079 Post-processing: Maximum Match 0% A277841 IM00141009 Maximum Match 100% A0112291 AU0112291 Listing first 45 summaries A2346440 IM0082016 Database : EST: 1: em_estba: * C 30 7.4 82.2 28 12 A2346840 2: em_estbum: * C 31 7.4 82.2 28 12 A2609297 3: em.estin: * C 32 7.4 82.2 28 12 A2514399 4: em.estmu: * C 33 7.4 82.2 29 12 A2602086 5: em.estov: * C 34 7.4 82.2 29 12 A2778941 6: em.estpl: * C 35 7.4 82.2 30 12 A2778941 7: em.estro: * C 36 7.4 82.2 31 12 A2510129 8: em_htc: * C 37 7.4 82.2 32 12 A2473867 9: gb.est1: * C 38 7.4 82.2 33 12 A2489350 10: gb.est2: * C 39 7.4 82.2 34 12 A2818898 11: gb_htc: * C 40 7.4 82.2 35 12 A285213 12: gb_gss: * C 41 7.4 82.2 36 12 A2510129 13: em_gss_hum: * C 42 7.4 82.2 37 12 A2510129 14: em_gss_inv: * C 43 7.4 82.2 38 12 A2488178 15: em_gss_pln: * C 44 7.4 82.2 39 12 A2595078 16: em_gss_vrt: * C 45 7.4 82.2 40 12 A280640 qx13d05.X ALIGMENTS									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
RESULT NO.	Score	Query Length	DB ID	Description	REFERENCE	AUTHORS	VERSION	KEYWORDS	ORGANISM
1	9	100.0	29	AZ818898 2M0098N1F	AZ818898	Dunn,D., Aoyagi,A., Barber,M., Beacons,T., Duval,B., Hamil,C., Reilly,Islam,H., Longacre,S., Mahmoud,M., Meenah,E., Pedersen,T., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nedderhausern,A. and Wright,D., Weiss,R.	20-FEB-2000	GSS: AZ818898.1 GI:12988806	Mus musculus
2	8	88.9	19	AZ2313531	LOCUS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammali; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; Mus, Mus musculus	2M0098N1F	DEFINITION	29 bp DNA sequence.
3	8	88.9	20	AZ230578	ACCESSION	AZ818898	AZ818898	KEYWORDS	
4	8	88.9	24	AZ819888	VERSION		AZ78025	SOURCE	
5	8	88.9	26	AZ2313876	KEYWORDS		AZ78243	ORGANISM	house mouse.
6	8	88.9	27	AZ2387860	REFERENCE		AZ826828	ORGANISM	
7	8	88.9	28	AZ648296	AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacons,T., Duval,B., Hamil,C., Reilly,Islam,H., Longacre,S., Mahmoud,M., Meenah,E., Pedersen,T., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nedderhausern,A. and Wright,D., Weiss,R.	AZ2387860	TITLE	
8	8	88.9	30	AZ2514561	COMMENT	Unpublished (2000)	AZ2399220	FEATURES	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
9	7.4	82.2	19	AZ2399220	CONTACT	Contact: Robert B. Weiss	AZ835621	FEATURES	University of Utah Genome Center
10	7.4	82.2	19	AZ810627	JOURNAL	Robert B. Weiss	AZ2468141	FEATURES	University of Utah
11	7.4	82.2	19	AZ2835621	COMMENT	University of Utah	AZ2468141 IM0281D04	FEATURES	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
12	7.4	82.2	21	AZ2468141	COMMENT	84112, USA	AZ360212 IM0103K04	FEATURES	Tel: 801 585 5606
13	7.4	82.2	22	AZ2430664	COMMENT	Fax: 801 585 7177	AZ2430664 IM0215D17	FEATURES	Email: ddunn@genetics.utah.edu
14	7.4	82.2	22	AZ2457101	COMMENT	Insert Length: 10000 Std Error: 0.00	AZ2457101 IM0260017	FEATURES	Plate: 0089 Row: N Column: 11
15	7.4	82.2	22	AZ2457101	COMMENT	Seq primer: CGTTGTAACAGACGCCGT	AZ475999 T. brucei	FEATURES	Class: plasmid ends
16	7.4	82.2	23	AZ2388663	COMMENT	High quality sequence stop: 29.	AZ2388663 IM0140J15	FEATURES	Location/Qualifiers
17	7.4	82.2	23	AZ2388663	COMMENT	1. .29	AZ2388663 IM0140J15	FEATURES	/organism="Mus musculus"
						/strain="C57BL/6J"			/db_xref="Taxon:10090"
						/clone="UUGC2M0089N11"			/clone_11b="Mouse 10kb plasmid UGGCIM library"

/clone="UUGCCIM003H07"
 /clone="Mouse 10kb plasmid UGGCIM library"
 /clone="UUGCCM0091H18"
 /clone="Mouse 10kb plasmid UGGCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XLI0-Gold, T1-resistant, F-"
 /note="Vector: PWD2Bv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnars/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XLI0-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT
 ORIGIN
 8 a 2 c 3 g 7 t

 RESULT 4
 Query Match 88.9%; Score 8; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 ttctgaga 9
 Db 10 TCTGAGA 17

 LOCUS AZ819888
 DEFINITION 2M0091H18R Mouse 10kb plasmid UGGCIM library Mus musculus genomic
 CLONE UUGC2M0091H18 R, DNA sequence.
 ACCESSION AZ819888.1
 VERSION GI:12989796
 KEYWORDS GSS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0091 row: H column: 18
 Seq primer: CACAGGGAACAGCTATGACC
 Class: Plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers 1..24

 /organism="Mus musculus"
 /strain="C57BL/6J"

 FEATURES source

 BASE COUNT
 ORIGIN
 6 a 5 c 5 g 8 t

 RESULT 5
 Query Match 88.9%; Score 8; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ttctgaga 8
 Db 14 TCTGAGA 21

 LOCUS AZ313876/c
 DEFINITION 1M030H21F Mouse 10kb Plasmid UGGCIM library Mus musculus genomic
 CLONE UGGCIM030H21 F, DNA sequence.
 ACCESSION AZ313876
 VERSION AZ313876.1
 KEYWORDS GSS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0091 row: H column: 21
 Seq primer: CGTTGAAACGAGGCCACT
 Class: Plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers 1..26

 FEATURES source

 /organism="Mus musculus"

source

1. .28
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCIM0317E15"
 /clone.lib="Mouse 10kb plasmid UGGCIM library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42av; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.Jax.org/resources/documents/dnare/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMW42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptored vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 88.9%; Score 8; DB 12; Length 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 tctgagaa 9
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 Db 17 tcTGAGAA 24

RESULT

8

A2514561

LOCUS A2514561 30 bp DEFINITION Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UGGCIM031N07 F, DNA sequence.

ACCESSION A2514561

VERSION A2514561.1

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 30)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

Title

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Comment

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Tel: 801 585 5506

Fax: 801 585 7177

Email: dnurn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0361 row: N column: 07

Seq Primer: CGTGTAAACGAGCGGCACT

Class: plasmid ends

High quality sequence stop: 30.

FEATURES SOURCE

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 /organism="Mus musculus"

/strain="C57BL/6J"
 /db_xref="taxon:10090"

/clone="UGGCIM031N07"
 /clone.lib="Mouse 10kb plasmid UGGCIM library"

/sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42av; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.Jax.org/resources/documents/dnare/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMW42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 88.9%; Score 8; DB 12; Length 30;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 tctgagaa 9
 |||||
 Db 17 tcTGAGAA 10

RESULT

9

A2399220

LOCUS A2399220 19 bp DEFINITION Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UGGCIM0164P23 R, DNA sequence.

ACCESSION A2399220

VERSION A2399220.1

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

Title

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Comment

Contact: Robert B. Weiss

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Email: dnurn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0164 row: P column: 23

Seq Primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

FEATURES	source	High quality sequence stop: 19. Location/Qualifiers
		1. 19
/organism	"Mus musculus"	
/strain	"C57BL/6J"	
/clone	"UUGC1M0156423"	
/clone_id	"Mouse 10kb plasmid UGGC1M library"	
/sex	"Male"	
/lab_host	"E. coli strain XL10-Gold, T1-resistant, F-"	
/note	"Vector: PWD2nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://wwwjax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 4732114 gb AF128072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor-modified mouse DNA was annealed to purified adaptors complementary to the insert adaptors and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
BASE COUNT	4 a 2 c 4 g 9 t	
ORIGIN		
FEATURES	source	High quality sequence stop: 19. Location/Qualifiers
		1. 19
/organism	"Mus musculus"	
/strain	"C57BL/6J"	
/db_xref	"taxon:10090"	
/clone	"UUGC2M0076H17"	
/clone_id	"Mouse 10kb plasmid UGGC1M library"	
/sex	"Male"	
/lab_host	"E. coli strain XL10-Gold, T1-resistant, F-"	
/note	"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://wwwjax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 4732114 gb AF129071.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor-modified mouse DNA was annealed to purified adaptors complementary to the insert adaptors and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
BASE COUNT	6 a 5 c 1 g 7 t	
ORIGIN		
FEATURES	source	Class: Plasmid ends High quality sequence stop: 19.
		Location/Qualifiers
RESULT	10	
LOCUS	AZ810627/c	
DEFINITION	2M0076H17F MOUSE 10kb plasmid UGGC1M library Mus musculus genomic	
ACCESION	AZ810627	
VERSION	AZ810627.1	
KEYWORDS	GSS.	
KEYWORDS	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 19)	
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Ross, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dawne@genetics.utah.edu Insert length: 10000 Std Error: 0.00	
RESULT	11	
LOCUS	AZ835621	
DEFINITION	2M0129L1R Mouse 10kb plasmid UGGC1M library Mus musculus genomic	
ACCESION	AZ835621	
VERSION	AZ835621.1	
KEYWORDS	GSS.	
KEYWORDS	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 19)	
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Ross, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	
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COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dawne@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0129 row: L column: 21	

		Plate: 0281	row: D	column: 04
		Seq primer:	CACACAGGAAACAGCTATGACC	
FEATURES	source	Class:	plasmid ends	
High quality sequence		Class:	plasmid ends	
Location/Qualifiers		High quality sequence stop:	20.	
1. .19		Location/Qualifiers		
		/organism="Mus musculus"		
		/strain="C57BL/6J"		
		/db_xref="taxon:10090"		
		/clone_id="UUGCIM0281m04"		
		/sex="Male"		
		/lab_host="E. coli strain XL10-Gold, β -lactamase, F+"		
		/note="Vector: PWD2Nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.Jax.org/resources/documents/dnarecs/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
BASE COUNT	6 a	3 c	3 g	7 t
ORIGIN				
		Query Match	82.2%	Score 7.4; DB 12; length 19;
		Best Local Similarity	88.9%	Pred. No. 7, 2e+05; Matches 8; Conservative 1; Indels 0; Gaps 0;
Qy	1 ttctggaaa	9		
Db	2 TTTCTGGAAA	10		
RESULT	12			
A2468141	A2468141	20 bp	DNA	linear GSS 04-OCT-2000
LOCUS	1M0281D04F	Mouse 10kb plasmid UGGCIM library	Mus musculus	genomic clone UGGCIM0281D04 F, DNA sequence.
DEFINITION	A2468141			
ACCESSION	A2468141.1			
VERSION	G1:10626266			
KEYWORDS	GSS.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 20)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.			
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Plasmid Inserts				
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss			
University of Utah Genome Center				
University of Utah				
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84112, USA				
Tel: 801 585 5606				
Fax: 801 585 7177				
Email: dounn@genetics.utah.edu				
Insert Length: 10000	Std Error: 0.00			
		Plate: 0281	row: D	column: 04
		Seq primer:	CCTTGAAACGCCCACT	
FEATURES	source	Class:	plasmid ends	
High quality sequence		Class:	plasmid ends	
Location/Qualifiers		High quality sequence stop:	20.	
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		/organism="Mus musculus"		
		/strain="C57BL/6J"		
		/db_xref="taxon:10090"		
		/clone_id="UUGCIM0281m04"		
		/sex="Male"		
		/lab_host="E. coli strain XL10-Gold, β -lactamase, F+"		
		/note="Vector: PWD2Nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.Jax.org/resources/documents/dnarecs/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
BASE COUNT	7 a	0 c	4 g	9 t
ORIGIN				
		Query Match	82.2%	Score 7.4; DB 12; length 20;
		Best Local Similarity	88.9%	Pred. No. 7, 2e+05; Matches 8; Conservative 1; Indels 0; Gaps 0;
Qy	1 ttctggaaa	9		
Db	7 TTATGAGAA	15		
RESULT	13			
A2360212	AZ360212	21 bp	DNA	linear GSS 02-OCT-2000
LOCUS	1M013K04F	Mouse 10kb plasmid UGGCIM library	Mus musculus	genomic clone UGGCIM013K04 F, DNA sequence.
DEFINITION	AZ360212			
ACCESSION	AZ360212.1			
VERSION	G1:10473912			
KEYWORDS	GSS.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 21)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.			
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84112, USA				
Tel: 801 585 5606				
Fax: 801 585 7177				
Email: dounn@genetics.utah.edu				

Insert length: 10000 Std Error: 0.00
 Plate: 0103 row: K column: 04
 Seq primer: CGTGTGAAACGACGGCCAGT
 Class: Plasmid ends
 High quality sequence stop: 21.

FEATURES source

Location/Qualifiers

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/sex="Male"

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UFGCIM0103K04"

/clone_1.lib="Mouse 10kb plasmid UFGCIM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F+"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnare/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|473211|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Fax: 801 585 7177
 Email: daunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0260 row: J column: 17
 Seq primer: CGTTGTAACGAGGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES

source

Location/Qualifiers
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 /strain="C57BL/6J"
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 /clone="UUGC1M0260J17"
 /clone_1b="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T₁-resistant, F₋"
 /note="vector: pMD42mv; Purified genomic DNA from M.
musculus C57BL/6J (male); Purified from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.Jax.org/resources/documents/dnarefs/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T₄ DNA Polymerase and T₄
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1|473214|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT

ORIGIN

Query Match	Score	DB	Length	Matches	Pred. No.	Mismatches	Indels	Gaps	Ov	Db
Best Local Similarity	82.2%	12	22	8; Conservative	7.3e+05	0	1	0	ttctggaa	ttttGAGAA
Matches	88.9%								9	7

Search completed: August 20, 2002, 22:51:42
 Job time: 5128 sec

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